

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/777, 186

Source: _____

Date Processed by STIC: _____

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IFWO

RAW SEQUENCE LISTING

DATE: 10/18/2004

PATENT APPLICATION: US/10/777,186

TIME: 09:17:36

Input Set : N:\Crf3\RULE60\10777186.raw.txt

Output Set: N:\CRF4\10182004\J777186.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Schlessinger, Joseph

6 Sap, Jan M.

8 (ii) TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE

9 PHOSPHATASE-ALPHA

11 (iii) NUMBER OF SEQUENCES: 14

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: PENNIE & EDMONDS

15 (B) STREET: 1155 AVENUE OF THE AMERICAS

16 (C) CITY: NEW YORK

17 (D) STATE: NEW YORK

18 (E) COUNTRY: U.S.A.

19 (F) ZIP: 10036

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/10/777,186

C--> 29 (B) FILING DATE: 13-Feb-2004

30 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

W--> 33 (A) APPLICATION NUMBER: US/09/280,597

34 (B) FILING DATE: 29-MARCH-1999

W--> 35 (A) APPLICATION NUMBER: US 08/015,985

36 (B) FILING DATE: 10-FEB-1993

38 (viii) ATTORNEY/AGENT INFORMATION:

39 (A) NAME: Coruzzi, Laura A.

40 (B) REGISTRATION NUMBER: 30,742

41 (C) REFERENCE/DOCKET NUMBER: 7683-020

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: (212) 790-9090

45 (B) TELEFAX: (212) 869-9741/8864

46 (C) TELEX: 66141 PENNIE

50 (2) INFORMATION FOR SEQ ID NO: 1:

52 (i) SEQUENCE CHARACTERISTICS:

53 (A) LENGTH: 802 amino acids

54 (B) TYPE: amino acid

55 (D) TOPOLOGY: linear

57 (ii) MOLECULE TYPE: protein

59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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61 Met Asp Ser Trp Phe Ile Leu Val Leu Leu Gly Ser Gly Leu Ile Cys
62   1           5           10           15
64 Val Ser Ala Asn Asn Ala Thr Thr Val Ala Pro Ser Val Gly Ile Thr
65           20           25           30
67 Arg Leu Ile Asn Ser Ser Thr Ala Glu Pro Val Lys Glu Glu Ala Lys
68           35           40           45
70 Thr Ser Asn Pro Thr Ser Ser Leu Thr Ser Leu Ser Val Ala Pro Thr
71           50           55           60
73 Phe Ser Pro Asn Ile Thr Leu Gly Pro Thr Tyr Leu Thr Thr Val Asn
74   65           70           75           80
76 Ser Ser Asp Ser Asp Asn Gly Thr Thr Arg Thr Ala Ser Thr Asn Ser
77           85           90           95
79 Ile Gly Ile Thr Ile Ser Pro Asn Gly Thr Trp Leu Pro Asp Asn Gln
80           100          105          110
82 Phe Thr Asp Ala Arg Thr Glu Pro Trp Glu Gly Asn Ser Ser Thr Ala
83           115          120          125
85 Ala Thr Thr Pro Glu Thr Phe Pro Pro Ser Gly Asn Ser Asp Ser Lys
86           130          135          140
88 Asp Arg Arg Asp Glu Thr Pro Ile Ile Ala Val Met Val Ala Leu Ser
89  145          150          155          160
91 Ser Leu Leu Val Ile Val Phe Ile Ile Ile Val Leu Tyr Met Leu Arg
92           165          170          175
94 Phe Lys Lys Tyr Lys Gln Ala Gly Ser His Ser Asn Ser Phe Arg Leu
95           180          185          190
97 Ser Asn Gly Arg Thr Glu Asp Val Glu Pro Gln Ser Val Pro Leu Leu
98           195          200          205
100 Ala Arg Ser Pro Ser Thr Asn Arg Lys Tyr Pro Pro Leu Pro Val Asp
101          210          215          220
103 Lys Leu Glu Glu Glu Ile Asn Arg Arg Met Ala Asp Asp Asn Lys Leu
104  225          230          235          240
106 Phe Arg Glu Glu Phe Asn Ala Leu Pro Ala Cys Pro Ile Gln Ala Thr
107           245          250          255
109 Cys Glu Ala Ala Ser Lys Glu Glu Asn Lys Glu Lys Asn Arg Tyr Val
110           260          265          270
112 Asn Ile Leu Pro Tyr Asp His Ser Arg Val His Leu Thr Pro Val Glu
113           275          280          285
115 Gly Val Pro Asp Ser Asp Tyr Ile Asn Ala Ser Phe Ile Asn Gly Tyr
116           290          295          300
118 Gln Glu Lys Asn Lys Phe Ile Ala Ala Gln Gly Pro Lys Glu Glu Thr
119  305          310          315          320
121 Val Asn Asp Phe Trp Arg Met Ile Trp Glu Gln Asn Thr Ala Thr Ile
122           325          330          335
124 Val Met Val Thr Asn Leu Lys Glu Arg Lys Glu Cys Lys Cys Ala Gln
125           340          345          350
127 Tyr Trp Pro Asp Gln Gly Cys Trp Thr Tyr Gly Asn Ile Arg Val Ser
128           355          360          365
130 Val Glu Asp Val Thr Val Leu Val Asp Tyr Thr Val Arg Lys Phe Cys
131           370          375          380
133 Ile Gln Gln Val Gly Asp Met Thr Asn Arg Lys Pro Gln Arg Leu Ile

```

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134	385				390				395				400			
136	Thr	Gln	Phe	His	Phe	Thr	Ser	Trp	Pro	Asp	Phe	Gly	Val	Pro	Phe	Thr
137				405						410					415	
139	Pro	Ile	Gly	Met	Leu	Lys	Phe	Leu	Lys	Lys	Val	Lys	Ala	Cys	Asn	Pro
140				420					425					430		
142	Gln	Tyr	Ala	Gly	Ala	Ile	Val	Val	His	Cys	Ser	Ala	Gly	Val	Gly	Arg
143			435					440					445			
145	Thr	Gly	Thr	Phe	Val	Val	Ile	Asp	Ala	Met	Leu	Asp	Met	Met	His	Thr
146		450					455					460				
148	Glu	Arg	Lys	Val	Asp	Val	Tyr	Gly	Phe	Val	Ser	Arg	Ile	Arg	Ala	Gln
149	465				470					475					480	
151	Arg	Cys	Gln	Met	Val	Gln	Thr	Asp	Met	Gln	Tyr	Val	Phe	Ile	Tyr	Gln
152				485					490					495		
154	Ala	Leu	Leu	Glu	His	Tyr	Leu	Tyr	Gly	Asp	Thr	Glu	Leu	Glu	Val	Thr
155			500						505				510			
157	Ser	Leu	Glu	Thr	His	Leu	Gln	Lys	Ile	Tyr	Asn	Lys	Ile	Pro	Gly	Thr
158		515						520					525			
160	Ser	Asn	Asn	Gly	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Thr	Ser	Ile	Lys	
161		530				535					540					
163	Ile	Gln	Asn	Asp	Lys	Met	Arg	Thr	Gly	Asn	Leu	Pro	Ala	Asn	Met	Lys
164	545				550					555					560	
166	Lys	Asn	Arg	Val	Leu	Gln	Ile	Ile	Pro	Tyr	Glu	Phe	Asn	Arg	Val	Ile
167				565					570					575		
169	Ile	Pro	Val	Lys	Arg	Gly	Glu	Glu	Asn	Thr	Asp	Tyr	Val	Asn	Ala	Ser
170			580						585				590			
172	Phe	Ile	Asp	Gly	Tyr	Arg	Gln	Lys	Asp	Ser	Tyr	Ile	Ala	Ser	Gln	Gly
173			595				600						605			
175	Pro	Leu	Leu	His	Thr	Ile	Glu	Asp	Phe	Trp	Arg	Met	Ile	Trp	Glu	Trp
176		610				615					620					
178	Lys	Ser	Cys	Ser	Ile	Val	Met	Leu	Thr	Glu	Leu	Glu	Glu	Arg	Gly	Gln
179	625				630					635					640	
181	Glu	Lys	Cys	Ala	Gln	Tyr	Trp	Pro	Ser	Asp	Gly	Leu	Val	Ser	Tyr	Gly
182				645					650					655		
184	Asp	Ile	Thr	Val	Glu	Leu	Lys	Lys	Glu	Glu	Glu	Cys	Glu	Ser	Tyr	Thr
185				660					665				670			
187	Val	Arg	Asp	Leu	Leu	Val	Thr	Asn	Thr	Arg	Glu	Asn	Lys	Ser	Arg	Gln
188			675					680				685				
190	Ile	Arg	Gln	Phe	His	Phe	His	Gly	Trp	Pro	Glu	Val	Gly	Ile	Pro	Ser
191		690				695					700					
193	Asp	Gly	Lys	Gly	Met	Ile	Ser	Ile	Ile	Ala	Ala	Val	Gln	Lys	Gln	Gln
194	705				710					715					720	
196	Gln	Gln	Ser	Gly	Asn	His	Pro	Ile	Thr	Val	His	Cys	Ser	Ala	Gly	Ala
197				725					730				735			
199	Gly	Arg	Thr	Gly	Thr	Phe	Cys	Ala	Leu	Ser	Thr	Val	Leu	Glu	Arg	Val
200			740					745				750				
202	Lys	Ala	Glu	Gly	Ile	Leu	Asp	Val	Phe	Gln	Thr	Val	Lys	Ser	Leu	Arg
203			755				760					765				
205	Leu	Gln	Arg	Pro	His	Met	Val	Gln	Thr	Leu	Glu	Gln	Tyr	Glu	Phe	Cys
206		770				775					780					

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208 Tyr Lys Val Val Gln Glu Tyr Ile Asp Ala Phe Ser Asp Tyr Ala Asn
 209 785 790 795 800

211 Phe Lys

214 (2) INFORMATION FOR SEQ ID NO: 2:

216 (i) SEQUENCE CHARACTERISTICS:

217 (A) LENGTH: 2409 base pairs

218 (B) TYPE: nucleic acid

219 (C) STRANDEDNESS: double

220 (D) TOPOLOGY: unknown

222 (ii) MOLECULE TYPE: cDNA

224 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

226	ATGGATTCTT	GGTTCATTCT	TGTTCTGCTC	GGCAGTGGTC	TGATATGTGT	CAGTGCCAAC	60
228	AATGCTACCA	CAGTTGCACC	TTCTGTAGGA	ATTACAAGAT	TAATTAACCT	ATCAACGGCA	120
230	GAACCAGTTA	AAGAAGAGGC	CAAAACTTCA	AATCCAACCT	CTTCACTAAC	TTCTCTTTCT	180
232	GTGGCACCAA	CATTCAGCCC	AAATATAACT	CTGGGACCCA	CCTATTTAAC	CACTGTCAAT	240
234	TCTTCAGACT	CTGACAATGG	GACCACAAGA	ACAGCAAGCA	CCAATTCTAT	AGGCATTACA	300
236	ATTTACACAA	ATGGAACGTG	GCTTCCAGAT	AACCAGTTCA	CGGATGCCAG	AACAGAACCC	360
238	TGGGAGGGGA	ATTCCAGCAC	CGCAGCAACC	ACTCCAGAAA	CTTTCCCTCC	TTCAGGTAAT	420
240	TCTGACTCGA	AGGACAGAAG	AGATGAGACA	CCAATTATTG	CGGTGATGGT	GGCCCTGTCC	480
242	TCTCTGCTAG	TGATCGTGTT	TATTATCATA	GTTTTGTACA	TGTTAAGGTT	TAAGAAATAC	540
244	AAGCAAGCTG	GGAGCCATTC	CAATTCTTTC	CGCTTATCCA	ACGGCCGCAC	TGAGGATGTG	600
246	GAGCCCCAGA	TGTGTCCACT	TCTGGCCAGA	TCCCCAAGCA	CCAACAGGAA	ATACCCACCC	660
248	CTGCCCGTGG	ACAAGCTGGA	AGAGGAAATT	AACCGGAGAA	TGGCAGACGA	CAATAAGCTC	720
250	TTCAGGGAGG	AATTCAACGC	TCTCCCTGCA	TGTCCTATCC	AGGCCACCTG	TGAGGCTGCT	780
252	TCCAAGGAGG	AAAACAAGGA	AAAAAATCGA	TATGTAAACA	TCTTGCCTTA	TGACCACTCT	840
254	AGAGTCCACC	TGACACCGGT	TGAAGGGGTT	CCAGATTCTG	ATTACATCAA	TGCTTCATTC	900
256	ATCAACGGTT	ACCAAGAAAA	GAACAAATTC	ATTGCTGCAC	AAGGACCAAA	AGAAGAAACG	960
258	GTGAATGATT	TCTGGCGGAT	GATCTGGGAA	CAAAACACAG	CCACCATCGT	CATGGTTACC	1020
260	AACCTGAAGG	AGAGAAAAGGA	GTGCAAGTGC	GCCCAGTACT	GGCCAGACCA	AGGCTGCTGG	1080
262	ACCTATGGGA	ATATTCGGGT	GTCTGTAGAG	GATGTGACTG	TCCTGGTGGA	CTACACAGTA	1140
264	CGGAAGTTCT	GCATCCAGCA	GGTGGGCGAC	ATGACCAACA	GAAAGCCACA	GCGCCTCATC	1200
266	ACTCAGTTCC	ACTTTACCAG	CTGGCCAGAC	TTTGGGGTGC	CTTTTACCCC	GATCGGCATG	1260
268	CTCAAGTTCC	TCAAGAAGGT	GAAGGCCTGT	AACCCTCAGT	ATGCAGGGGC	CATCGTGGTC	1320
270	CACTGCAGTG	CAGGTGTAGG	GCGTACAGGT	ACCTTTGTCT	TCATTGATGC	CATGCTGGAC	1380
272	ATGATGCATA	CAGAACGGAA	GGTGGACGTG	TATGGCTTTG	TGAGCCGGAT	CCGGGCACAG	1440
274	CGCTGCCAGA	TGGTGCAAAC	CGATATGCAG	TATGTCTTCA	TATACCAAGC	CCTTCTGGAG	1500
276	CATTATCTCT	ATGGAGATAC	AGAAGTGGAA	GTGACCTCTC	TAGAAACCCA	CCTGCAGAAA	1560
278	ATTTACAACA	AAATCCAGAG	GACCAGCAAC	AATGGATTAG	AGGAGGAGTT	TAAGAAGTTA	1620
280	ACATCAATCA	AAATCCAGAA	TGACAAGATG	CGGACTGGAA	ACCTTCCAGC	CAACATGAAG	1680
282	AAGAACCGTG	TTTTACAGAT	CATTCCATAT	GAATTCAACA	GAGTGATCAT	TCCAGTTAAG	1740
284	CGGGGCGAAG	AGAATACAGA	CTATGTGAAC	GCATCCTTTA	TTGATGGCTA	CCGGCAGAAG	1800
286	GACTCCTATA	TCGCCAGCCA	GGGCCCTCTT	CTCCACACAA	TTGAGGACTT	CTGGCGAATG	1860
288	ATCTGGGAGT	GGAATCCTG	CTCTATCGTG	ATGCTAACAG	AACTGGAGGA	GAGAGGCCAG	1920
290	GAGAAGTGTG	CCCAGTACTG	GCCATCTGAT	GGACTGGTGT	CCTATGGAGA	TATTACAGTG	1980
292	GAACTGAAGA	AGGAGGAGGA	ATGTGAGAGC	TACACCGTCC	GAGACCTCCT	GGTCACCAAC	2040
294	ACCAGGGAGA	ATAAGAGCCG	GCAGATCCGG	CAGTTCCACT	TCCATGGCTG	GCCTGAAGTG	2100
296	GGCATCCCCA	GTGACGGAAA	GGGCATGATC	AGCATCATCG	CCGCCGTGCA	GAAGCAGCAG	2160
298	CAGCAGTCAG	GGAACACCCC	CATCACCGTG	CACTGCAGCG	CCGGGGCAGG	AAGGACGGGG	2220
300	ACCTTCTGTG	CCCTGAGCAC	CGTCTGGAG	CGTGTGAAAG	CAGAGGGGAT	TTTGGATGTC	2280

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302 TTCCAGACTG TCAAGAGCCT GCGGCTACAG AGGCCACACA TGGTCCAGAC ACTGGAACAG      2340
304 TATGAGTTCT GCTACAAGGT GGTGCAGGAG TATATTGATG CATTCTCAGA TTATGCCAAC      2400
306 TTCAAGTAA                                                                2409
309 (2) INFORMATION FOR SEQ ID NO: 3:
311     (i) SEQUENCE CHARACTERISTICS:
312         (A) LENGTH: 793 amino acids
313         (B) TYPE: amino acid
314         (D) TOPOLOGY: linear
316     (ii) MOLECULE TYPE: protein
318     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
320 Met Asp Ser Trp Phe Ile Leu Val Leu Phe Gly Ser Gly Leu Ile His
321   1           5           10           15
323 Val Ser Ala Asn Asn Ala Thr Thr Val Ser Pro Ser Leu Gly Thr Thr
324           20           25           30
326 Arg Leu Ile Lys Thr Ser Thr Thr Glu Leu Ala Lys Glu Glu Asn Lys
327   35           40           45
329 Thr Ser Asn Ser Thr Ser Ser Val Ile Ser Leu Ser Val Ala Pro Thr
330   50           55           60
332 Phe Ser Pro Asn Leu Thr Leu Glu Pro Thr Tyr Val Thr Thr Val Asn
333  65           70           75           80
335 Ser Ser His Ser Asp Asn Gly Thr Arg Arg Ala Ala Ser Thr Glu Ser
336           85           90           95
338 Gly Gly Thr Thr Ile Ser Pro Asn Gly Ser Trp Leu Ile Glu Asn Gln
339   100          105          110
341 Phe Thr Asp Ala Ile Thr Glu Pro Trp Glu Gly Asn Ser Ser Thr Ala
342   115          120          125
344 Ala Thr Thr Pro Glu Thr Phe Pro Pro Ala Asp Glu Thr Pro Ile Ile
345   130          135          140
347 Ala Val Met Val Ala Leu Ser Ser Leu Leu Val Ile Val Phe Ile Ile
348  145          150          155          160
350 Ile Val Leu Tyr Met Leu Arg Phe Lys Lys Tyr Lys Gln Ala Gly Ser
351   165          170          175
353 His Ser Asn Ser Phe Arg Leu Ser Asn Gly Arg Thr Glu Asp Val Glu
354   180          185          190
356 Pro Gln Ser Val Pro Leu Leu Ala Arg Ser Pro Ser Thr Asn Arg Lys
357   195          200          205
359 Tyr Pro Pro Leu Pro Val Asp Lys Leu Glu Glu Glu Ile Asn Arg Arg
360   210          215          220
362 Met Ala Asp Asp Asn Lys Leu Phe Arg Glu Glu Phe Asn Ala Leu Pro
363  225          230          235          240
365 Ala Cys Pro Ile Gln Ala Thr Cys Glu Ala Ala Ser Lys Glu Glu Asn
366           245          250          255
368 Lys Glu Lys Asn Arg Tyr Val Asn Ile Leu Pro Tyr Asp His Ser Arg
369           260          265          270
371 Val His Leu Thr Pro Val Glu Gly Val Pro Asp Ser Asp Tyr Ile Asn
372           275          280          285
374 Ala Ser Phe Ile Asn Gly Tyr Gln Glu Lys Asn Lys Phe Ile Ala Ala
375   290          295          300
377 Gln Gly Pro Lys Glu Glu Thr Val Asn Asp Phe Trp Arg Met Ile Trp

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; Xaa Pos.8,12,21,22,24,25,27,28,30,37,39,47,57,72,77,89,94,95,99,104
Seq#:9; Xaa Pos.109,111,115,116,124,125,131,133,135,137,138,139,143,144,153
Seq#:9; Xaa Pos.155,170,174,176,179,180,181,182,183,186,205,211,212,214,215
Seq#:9; Xaa Pos.217,222,227,230,232,240,244,247
Seq#:14; Xaa Pos.10,20,21,22,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38
Seq#:14; Xaa Pos.39,40,41,42,43,55,67,70,87,95,96,97,99,100,103,105,106,112
Seq#:14; Xaa Pos.114,115,116,120,121,123,126,127,128,133,137,138,139,141
Seq#:14; Xaa Pos.143,149,151,182,186,188,195,196,197,198,199,200,201,202
Seq#:14; Xaa Pos.205,209,212,213,214,218,222,224,228,229,244,247,254,257
Seq#:14; Xaa Pos.264,265,266,267

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10777186.raw.txt

Output Set: N:\CRF4\10182004\J777186.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:35 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)
L:836 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
M:341 Repeated in SeqNo=9
L:1142 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
M:341 Repeated in SeqNo=14